

EXHIBIT A

1. SEQ5 vs. SEQ2

Aligned Length = 81 Gaps = 1
Identities = 45 (55%) Similarities = 12 (14%)

```
SEQ5   1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ2   1 MRLALSGLLCMLLLCFCIFSSEGRHPAKSLKLRR---CCHLSPRSKLT 47
      **** ** ***.*****.***.***.***.   **   ***  *   *
```

```
SEQ5   51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ2   48 TWKGNHTRPCRLCRNKLPVKS WVVP GALPQI 78
      . **.* * * . * . *****.
```

2. SEQ5 vs. SEQ7

Aligned Length = 81 Gaps = 2
Identities = 38 (46%) Similarities = 11 (13%)

```
SEQ5   1 MRLVLSSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNST 50
SEQ7   1 MRLTL SGLFFMLFLCLCVLSSEGRKRP AKFPKL RP---RCHLSPRSKPI 47
      **** ** * . * ** .. *.***.*****   *   **  *
```

```
SEQ5   51 NLKGHHVRLCKPCKLEPEPRLWVVP GALPQV 81
SEQ7   48 TWKGNHTRPCRPCR-KLESNS WVVP GALPQI 77
      . **.* * * *.** . * *****.
```